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Sequences

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BLAST2 Manual

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Program: **blastp**
Sequence ID(s):
983910CD1 vs. genpept136

NCBI-BLASTP 2.0.10 [Aug-26-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 983910CD1
(314 letters)

Database: genpept136
1,453,555 sequences; 449,659,834 total letters

Searching.....done

Sequences producing significant alignments:		Score	E
		(bits)	Value
<input checked="" type="checkbox"/>	g3002935 T cell receptor beta chain [Homo sapiens]	550	e-155
<input checked="" type="checkbox"/>	g1100182 T-cell receptor beta [Homo sapiens]	546	e-154
<input checked="" type="checkbox"/>	g139012 T-cell receptor precursor [Homo sapiens]	522	e-147
<input checked="" type="checkbox"/>	g6741519 unnamed protein product (unidentified)	490	e-137
<input checked="" type="checkbox"/>	g29469988 T cell receptor beta chain BV12S1 J1-1 BC1 [Homo sa	490	e-137
>g3002935 T cell receptor beta chain [Homo sapiens]		Length = 309	

Score = 550 bits (1401), Expect = e-155
Identities = 272/311 (87%), Positives = 280/311 (89%), Gaps = 3/311 (0%)
Query: 1 MNTLLQWALCLLGADHTGAGVSGTSPKRVTEKGVKVELRCDPISGHTALWYTRSLQ 60
Sbjct: 1 MNTLLQWALCLLGADHTGAGVSGTSPKRVTEKGVKVELRCDPISGHTALWYTRSLQ 60

Query: 61 GFEFLTYFGTGAADSGLRNDRFPNRPSSVSTLKIQTQEDSAAVLRAGVAGMS 120
G EFLTYFG A D SGLPDRF A R GSVSTL IQTQ Q DSA YL A + S
Sbjct: 61 GLEFLTYFGNSAPKSGELPDRFSAERTGSGVSTLTITQTQEDSNAVIL--CASSLSL 117
Query: 121 YNEQYFGTRULVLELKNFPEFVAVFEPSEAEISHTQKATVCLATGCFYDHELSW 180
+ +FC GTRULV EDL VFPFVAVFEPSEAEISHTQKATVCLATG +FDHELSW
Sbjct: 118 LSEPLFGNTRULVTEDEAKVFPFVAVFEPSEAEISHTQKATVCLATGCFYDHELSW 177
Query: 181 WNKKEVHSGVSTDQPLKEQPALANDSRVCLSSRLRVSAATFWQNFNFRFCQVQYGLSE 240
WNKKEVHSGVSTDQPLKEQPALANDSRVCLSSRLRVSAATFWQNFNFRFCQVQYGLSE 237
Sbjct: 178 WNKKEVHSGVSTDQPLKEQPALANDSRVCLSSRLRVSAATFWQNFNFRFCQVQYGLSE 237
Query: 241 NDEMTQDRAKPVTVQVNSADWAGRADCGFTSSTQYQGVLSATILYELLGKATLVAVLSA 300
NDEMTQDRAKPVTVQVNSADWAGRADCGFTS STQYQGVLSATILYELLGKATLVAVLSA
Sbjct: 238 NDEMTQDRAKPVTVQVNSADWAGRADCGFTSVSYQGVLSATILYELLGKATLVAVLSA 297
Query: 301 LVLMAMVKKDSRG 311
LVLMAMVKKDSRG
Sbjct: 298 LVLMAMVKKDSRG 308

>g1100182 T-cell receptor beta [Homo sapiens]
Length = 311

Score = 546 bits (1391), Expect = e-154
Identities = 268/314 (85%), Positives = 282/314 (89%), Gaps = 3/314 (0%)

Query: 1 MNTLLQWALCLLGADHTGAGVSGTSPKRVTEKGVKVELRCDPISGHTALWYTRSLQ 60
MGT LLQW ALCLLGADH GVSQ P +K+T++G+V RCDPIS H LNWYRQ+LQ
Sbjct: 1 MNTSLLQWALCLLGADHTGAGVSGTSPKRVTEKGVKVELRCDPISGHTALWYTRSLQ 60

Query: 61 GFEFLTYFGTGAADSGLRNDRFPNRPSSVSTLKIQTQEDSAAVLRAGVAGMS 120
GFEEL YFG + S L +DRF A RP+GS STL+IQTQEDSA YL A ++ +S
Sbjct: 61 GFEFLTYFONEAQLEKSRLLSDRFSAERPKGSFTLEIQTQEDSNAVILCA--SSNGTS 118

Query: 121 YNEQYFGTRULVLELKNFPEFVAVFEPSEAEISHTQKATVCLATGCFYDHELSW 180
Y EQYFGTRULV EDLKNFPEFVAVFEPSEAEISHTQKATVCLATGCFYDHELSW
Sbjct: 119 Y-EQYFGTRULVTEDEAKVFPFVAVFEPSEAEISHTQKATVCLATGCFYDHELSW 177

Query: 181 WNKKEVHSGVSTDQPLKEQPALANDSRVCLSSRLRVSAATFWQNFNFRFCQVQYGLSE 240
WNKKEVHSGVSTDQPLKEQPALANDSRVCLSSRLRVSAATFWQNFNFRFCQVQYGLSE 237
Sbjct: 178 WNKKEVHSGVSTDQPLKEQPALANDSRVCLSSRLRVSAATFWQNFNFRFCQVQYGLSE 237

Query: 241 NDEMTQDRAKPVTVQVNSADWAGRADCGFTSSTQYQGVLSATILYELLGKATLVAVLSA 300
NDEMTQDRAKPVTVQVNSADWAGRADCGFTSSTQYQGVLSATILYELLGKATLVAVLSA
Sbjct: 238 NDEMTQDRAKPVTVQVNSADWAGRADCGFTSSTQYQGVLSATILYELLGKATLVAVLSA 297

Query: 301 LVLMAMVKKDSRG 311
LVLMAMVKKDSRG
Sbjct: 298 LVLMAMVKKDSRG 311

>g139012 T-cell receptor precursor [Homo sapiens]
Length = 310

Score = 522 bits (1330), Expect = e-147
Identities = 254/311 (81%), Positives = 271/311 (86%), Gaps = 2/311 (0%)

BLAST2 Results

http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer

BLAST2 Results

http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer

Query: 1 MGTLLQWALCLGADHTGAGVSGTSPNNKVTKEGVDVLRCDPISGHTALWVRQSLQ 60
MGT LLQW ALCLGADH GVSQ P + *T+G+V RCDPIS H LWMVRQ+LQ 60
Sbjct: 1 MGTSLQWALCLGADHADVTGVSQFNPNITKROQNTVTRCDPISGHTALWVRQSLQ 60
M T L-QWA LL A T V+QTPS++VT+ G+V LRC PIS H WVRQ LQ 60
Query: 61 GFEELVYQGTGAADSGLENDPFAVRPESGVSSTLKIQRTQDSAAVLRAGVAGNS 120
GFEEL YQ + S L +DRF A R+GS STL+IQRTQDSA YL A AG +
Sbjct: 61 GFEELVYQEAQLSKRLSDRFSABRPKGSFSTLEIQRTQDSAMYLCASSAGLNQ 120
Query: 121 YNEQYFGGTRLVLELANKVFPPEVAVFEPSEAEISHTQKATVCLATGCFYDHRVLSW 180
Q+FG GTRLV+LEL VFPPEVAVFEPSEAEISHTQKATVCLATG +FDRVLSW
Sbjct: 121 --PQIFGGTRLSLELANKVFPPEVAVFEPSEAEISHTQKATVCLATGCFYDHRVLSW 178
Query: 181 WNKKEVHSGVSTDPQLKEQPALANDSRVCLSSRLKRVSAFTWQNNHFRQCVQYGLSE 240
WNKKEVHSGVSTDPQLKEQPALANDSRVCLSSRLKRVSAFTWQNNHFRQCVQYGLSE
Sbjct: 179 WNKKEVHSGVSTDPQLKEQPALANDSRVCLSSRLKRVSAFTWQNNHFRQCVQYGLSE 238
Query: 241 NDEMTQDRAKPVTOIVSAEAWGRADCGFTS YQGGVLSATILYEILGKATVAVLSA 300
NDEMTQDRAKPVTOIVSAEAWGRADCGFTS YQGGVLSATILYEILGKATVAVLSA
Sbjct: 239 NDEMTQDRAKPVTOIVSAEAWGRADCGFTS YQGGVLSATILYEILGKATVAVLSA 298
Query: 301 LVLMAMVVRKD 311
LVLMAMVVRKD
Sbjct: 299 LVLMAMVVRKD 309
>6741519 unnamed protein product [unidentified]
Length = 311

Score = 490 bits (1249), Expect = e-137
Identities = 248/314 (78%), Positives = 267/314 (84%), Gaps = 3/314 (0%)
Query: 1 MGTLLQWALCLGADHTGAGVSGTSPNNKVTKEGVDVLRCDPISGHTALWVRQSLQ 60
M T L-QWA LL A T V+QTPS++VT+ G+V LRC PIS H WVRQ LQ 60
Sbjct: 1 MDTLVCAIFSLKAGLTEPVTQTSHQVQWQEVILRCVPISNHLYFWVRQILQ 60
Query: 61 GFEELVYQGTGAADSGLENDPFAVRPESGVSSTLKIQRTQDSAAVLRAGVAGNS 120
EPL+ F ++ S + +d+F R+GS TLKI+ T+ DSA Y A ++ +S
Sbjct: 61 KVEPLVSFNNELSEKSEIFDQFSEVERPQSNFTLKISTKLSDSNATPCA--SSEINS 118
Query: 121 YNEQYFGGTRLVLELANKVFPPEVAVFEPSEAEISHTQKATVCLATGCFYDHRVLSW 180
Y EQYFGGTRLV EDLKNVFPPEVAVFEPSEAEISHTQKATVCLATGCFYDHRVLSW
Sbjct: 119 Y-EQYFGGTRLVLELANKVFPPEVAVFEPSEAEISHTQKATVCLATGCFYDHRVLSW 177
Query: 181 WNKKEVHSGVSTDPQLKEQPALANDSRVCLSSRLKRVSAFTWQNNHFRQCVQYGLSE 240
WNKKEVHSGVSTDPQLKEQPALANDSRVCLSSRLKRVSAFTWQNNHFRQCVQYGLSE
Sbjct: 178 WNKKEVHSGVSTDPQLKEQPALANDSRVCLSSRLKRVSAFTWQNNHFRQCVQYGLSE 237
Query: 241 NDEMTQDRAKPVTOIVSAEAWGRADCGFTS YQGGVLSATILYEILGKATVAVLSA 300
NDEMTQDRAKPVTOIVSAEAWGRADCGFTS YQGGVLSATILYEILGKATVAVLSA
Sbjct: 238 NDEMTQDRAKPVTOIVSAEAWGRADCGFTS YQGGVLSATILYEILGKATVAVLSA 297
Query: 301 LVLMAMVVRKD 314
LVLMAMVVRKSG
Sbjct: 298 LVLMAMVVRKSG 311

>23469988 T cell receptor beta chain BV12s1 J1-1 BC1 [Homo sapiens]
Length = 309

Score = 490 bits (1249), Expect = e-137
Identities = 241/311 (77%), Positives = 262/311 (83%), Gaps = 3/311 (0%)
Query: 1 MGTLLQWALCLGADHTGAGVSGTSPNNKVTKEGVDVLRCDPISGHTALWVRQSLQ 60
M + C +LC+L A HT AGV Q+P ++VTE G+V LRC PISGH +L+VWRO++ +
Sbjct: 1 MDSMTFCVCSLCIIVAKHTDAGVTQSRUEVTEMQEVTLCCKPISGHSLSFWVRQWNR 60
Query: 61 GFEELVYQGTGAADSGLENDPFAVRPESGVSSTLKIQRTQDSAAVLRAGVAGNS 120
G E LTF DSG+P DRF A P S STKIQ +E DSA Y A+ ++
Sbjct: 61 GLELLYFNANNPIDDGSEHEDRFSANNPASFSTLKIQSEPHDSAVTF--CAGSFMG 117
Query: 121 YNEQYFGGTRLVLELANKVFPPEVAVFEPSEAEISHTQKATVCLATGCFYDHRVLSW 180
E +FG GTRLV+EDL VFPPEVAVFEPSEAEISHTQKATVCLATG+FDHRVLSW
Sbjct: 118 AGEAFFQGGTRLVTVVEDIANKVFPPEVAVFEPSEAEISHTQKATVCLATGCFYDHRVLSW 177
Query: 181 WNKKEVHSGVSTDPQLKEQPALANDSRVCLSSRLKRVSAFTWQNNHFRQCVQYGLSE 240
WNKKEVHSGVSTDPQLKEQPALANDSRVCLSSRLKRVSAFTWQNNHFRQCVQYGLSE
Sbjct: 178 WNKKEVHSGVSTDPQLKEQPALANDSRVCLSSRLKRVSAFTWQNNHFRQCVQYGLSE 237
Query: 241 NDEMTQDRAKPVTOIVSAEAWGRADCGFTS YQGGVLSATILYEILGKATVAVLSA 300
NDEMTQDRAKPVTOIVSAEAWGRADCGFTS YQGGVLSATILYEILGKATVAVLSA
Sbjct: 238 NDEMTQDRAKPVTOIVSAEAWGRADCGFTS YQGGVLSATILYEILGKATVAVLSA 297
Query: 301 LVLMAMVVRKD 311
LVLMAMVVRKD
Sbjct: 298 LVLMAMVVRKD 308

Database: genpept136
Posted date: Jul 31, 2003 9:27 AM
Number of letters in database: 449,659,834
Number of sequences in database: 1,453,555

Lambda K H 0.318 0.133 0.411
Gapped
Lambda K H 0.270 0.0470 0.230

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 297167763
Number of Sequences: 1453555
Number of extensions: 12787980
Number of successful extensions: 59096
Number of sequences better than 10.0: 17425
Number of HSP's better than 10.0 without gapping: 4379
Number of HSP's successfully gapped in prelim test: 13046
Number of HSP's that attempted gapping in prelim test: 48416
Number of HSP's gapped (non-prelim): 19060
Length of query: 314
Length of database: 449,659,834
effective HSP length: 56
effective length of query: 258
effective length of database: 368,260,754
effective search space: 95011274532
effective search space used: 95011274532

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 41 (21.7 bits)

Submit sequences to:

